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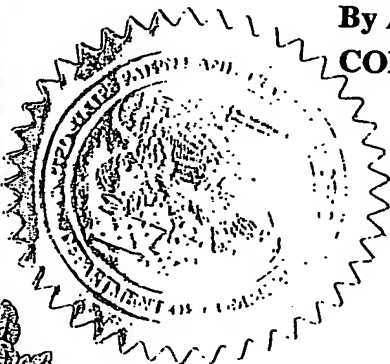
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PROVISIONAL APPLICATION COVER SHEET

Sir:

Transmitted herewith for filing is a **PROVISIONAL** patent application entitled: SAMPLE PREPARATION METHOD AND ARRANGEMENT THEREFOR

This provisional application includes:

1. XX A specification (24 pages)
2. XX 8 Sheets of drawings (Figs 1-9)
3. XX This application qualifies for small entity status.
4. XX A Credit Card Payment Form in the amount of  
— \$160.00 (large entity) or  
XX \$80.00 (small entity).

First Inventor: Jussi NURMI

Residence: Bodnäsän rantatie 72, FIN-21600 Parainen, Finland

Second Inventor: Teemu KORPIMÄKI

Residence: Bilmarkinkatu 4 as. 11, FIN-20100 Turku, Finland

Third Inventor: \_\_\_\_\_

Residence: \_\_\_\_\_

Fourth Inventor: \_\_\_\_\_

Residence: \_\_\_\_\_

Fifth Inventor: \_\_\_\_\_

Residence: \_\_\_\_\_

Sixth Inventor: \_\_\_\_\_

Residence: \_\_\_\_\_

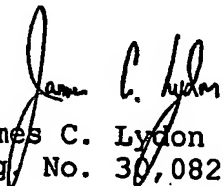
PROVISIONAL APPLICATION COVER SHEET

Please address all communications concerning this provisional application to:

James C. Lydon  
100 Daingerfield Road  
Suite 100  
Alexandria, VA 22314  
Telephone: (703) 838-0445  
Facsimile: (703) 838-0447

Please charge any additional required fees or credit any overpayment to our Deposit Account No. 50-1258. Two copies of this Provisional Application Cover Sheet are enclosed herewith.

Respectfully submitted,

  
James C. Lydon  
Reg. No. 30,082

Attorney Docket No.: TUR-154  
100 Daingerfield Road  
Suite 100  
Alexandria, VA 22314  
Telephone: (703) 838-0445  
Facsimile: (703) 838-0447

## **SAMPLE PREPARATION METHOD AND ARRANGEMENT THEREFOR**

### **FIELD OF THE INVENTION**

The present invention relates to a sample preparation method. The invention further relates to an arrangement for the method.

### **5 BACKGROUND OF THE INVENTION**

During the past few decades, tremendous advances have been made in the field of molecular diagnostics. Molecular recognition techniques such as immunoassay, the polymerase chain reaction and other nucleic acid amplification and detection methods have made it possible to specifically detect and quantify various biological  
10 entities – hereafter called analytes – in different kinds of samples. Measurement of the amount or mere presence of such analytes is of importance in a vast range of situations, examples of which include diagnosis and monitoring of disease in man or in animals; environmental monitoring; detection of biological warfare agents; forensic sciences and detection and recognition of cells and viruses. Developments  
15 in different aspects of these molecular recognition techniques – instrumentation, label technologies, reagents and consumables – have made it possible to detect even minute amounts of specific molecules of interest. Using the polymerase chain reaction (Saiki et al., Science 1985, 230: p. 1350-4) coupled with a suitable detection method, for example, it is often possible to detect a single nucleic acid  
20 analyte molecule of a particular base sequence in the presence of a great excess of other sequences.

However, most molecular measurement techniques are limited by the fact that the sample material itself, from which the measurements are to be made, must be purified prior to analysis. This is due to the fact that many components of e.g. blood,

environmental or food samples can inhibit the enzymes used in analysis; interfere with the formation of bioaffinity bonds that are essential in most modern molecular assays; increase the background signal obtained in the measurement step; or otherwise compromise assay performance. This is particularly true for nucleic acid assays, where the first step is usually DNA or RNA extraction (Lantz et al. Biotechnol. Annu. Rev. 2000: 5 p. 87-130). Common methods of sample preparation have been reviewed recently by Rådström et al. [Sachse K & Frey J (ed.), Methods in molecular biology, Vol 216: PCR detection of microbial pathogens, Humana Press Inc., Totowa, USA: p. 31-50]. These include biochemical methods based on, for example, extraction of nucleic acids using organic solvents, followed by ethanol precipitation and solubilisation in an aqueous solvent; or lysis of cells in the presence of chaotropic salts, affinity binding of the nucleic acids on a solid phase; and elution of pure nucleic acids using an aqueous solvent. The main advantage of these biochemical extraction methods is that the analyte is obtained in a pure form without any assay inhibitors. However, all of these methods present a real challenge to automation, are labour intensive and require specialized, expensive equipment together with harsh chemicals that cannot be used in, for example, field conditions.

In addition to the possibility of assay inhibition, sample volume itself is often a problem. Even if a sensitive assay is capable of detecting a single analyte molecule, this is sometimes not enough. For example, according to regulations concerning some pathogenic organisms, such as bacteria belonging to the genera *Salmonella* or *Listeria*, foodstuff must not contain more than a single viable bacterial cell in 25 g of the foodstuff. The amount of sample – 25 g – is far too great to be analysed in one bioaffinity reaction. For this reason, the analyte must be concentrated or/and enriched prior to analysis. Analyte concentration can be done by immunological or/and physical means (see Rådström et al.). More often than not, physiological enrichment in selective culture media is used. Such enrichment usually takes between 24 and 48 hours. In many cases, the time needed to perform the analysis is

therefore very long, which results in significant storage costs before a product, e.g. animal feed product, can be released to market.

To simplify the sample pre-treatment protocols, several attempts have been made to develop methods where assay inhibitors would be removed without the need to extract DNA or RNA in a pure form and where the analyte would be concentrated to a detectable level. Mainly, these methods are based on enrichment of the target cells from a sample, after which the cells are subjected to analysis. Venkateswaran et al. (Applied and Environmental Microbiology 1997, 63: p. 4127-4131) described the use of centrifugation and filtration to extract bacterial cells that were subsequently subjected to analysis by PCR. Although this method allowed detection of bacterial cells in the absence of DNA extraction, it was limited in the sense that a centrifuge was needed, which makes the method poorly suited for automation or for use outside a laboratory. Also, in the method described by Venkateswaran et al., target cells were collected from the filter by resuspending them in a buffer, which may very well result in some cells being trapped on the filter. This means that the method does not allow quantitative determination of the amount of the target cells.

In summary, the use of sophisticated molecular recognition and quantitation techniques is usually only possible in specialized laboratories, because the purification and enrichment techniques that are required by most nucleic acid sequence and/or protein detection methods are labour intensive and need specialized equipment and operator skills.

Therefore, there is a need for simple, fast and inexpensive sample preparation methods that allow reduction of the amount of assay inhibitors in the sample together with concentration or enrichment of analyte molecules.

## OBJECTS AND SUMMARY OF THE INVENTION

An object of the present invention is to provide a simplified method for preparing a biological sample to enable an altogether simplified analysis of an analyte or analytes.

- 5 Another object of the present invention is to provide an arrangement for preparing a biological sample according to the method of the invention.

Still another object of the present invention is to provide a kit for analysis of an analyte or analytes comprising the arrangement for preparing a biological sample according to the method of the invention.

- 10 Thus the present invention provides a method for preparing a biological sample for quantitative and/or qualitative analysis of the presence of a specific analyte or specific analytes, which analytes, if present, are contained in biological particles of the sample, in which method the sample is forced in a first direction through a filter that retains said biological particles. Characteristic for the method is that the
- 15 biological particles retained in the filter are flushed, by a flush flow, in a second opposite direction through the filter out of the filter and the flush flow containing the biological particles flushed out is analysed for the analyte or analytes.

- The present invention further provides an arrangement for preparing a biological sample for quantitative and/or qualitative analysis of the presence of a specific
- 20 analyte or specific analytes, which analytes, if present, are contained in biological particles of the sample. Characteristic for the arrangement is that it comprises

- a) a housing for a filter;
- b) a filter within said housing for retaining the particles containing the analyte or analytes, said filter having two sides,
  - 25 i) a sample inlet side and
  - ii) a flushing flow inlet side; and

c) means for

- i) leading the sample through the filter from the sample inlet side to the flushing flow inlet side,
- ii) leading the flush flow from its inlet side to the sample inlet side, and
- 5 iii) retrieving for analysis biological particles containing the analyte flushed from the filter.

The present invention also provides a kit of parts, components and/or reagents for performing the method according to the invention. Characteristic for the kit is that it comprises the arrangement according to the invention.

## 10 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the basic principle of the invention.

Figure 2a and 2b schematically show the principle of the invention used with pre-filtration.

Figure 3a, 3b and 3c schematically show the principle of an automatic sample pre-treatment instrument utilizing the principles of the present invention.

Figure 4 shows a standard curve for the detection of *Listeria monocytogenes* from milk using the present invention for sample pre-treatment and real time PCR for analyte detection.

Figure 5 shows a standard curve for the detection of *Listeria monocytogenes* from cheese using the present invention for sample pre-treatment and real time PCR for analyte detection.



Figure 6 shows a standard curve for the detection of *Listeria monocytogenes* from salted salmon using the present invention for sample pre-treatment and real time PCR for analyte detection.

Figure 7 shows a standard curve for the detection of *Bacillus subtilis* from Luria broth using the present invention for sample pre-treatment and real time PCR for analyte detection.

Figure 8 shows a standard curve for the detection of *Bacillus subtilis* endospores from potato flour using the present invention for sample pre-treatment and real-time PCR for analyte detection.

Figure 9 shows a picture of an agarose gel analysis of the PCR amplifications of an actin fragment from human blood leucocytes isolated with the method of the present invention.

#### DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The object of the present invention is to provide a simple, fast and cost-effective sample preparation method that is amenable to automation as well as manual operation that allows purification and concentration of e.g. biological nucleic acid or protein analytes from biological, environmental or other liquid or gaseous samples. Gaseous and liquid samples are suitable as such whereas solid samples have first to be suspended in a liquid.

A seminal finding of the present invention is that target cells can be enriched and purified from assay inhibitors by using a filter that allows liquid or gas to be directed through the filter in two opposed directions: the sample is first forced through the filter in such a manner that the target cells or other biological complexes of interest are retained on and/or in the filter while any contaminating or inhibitory substances pass through, after which the direction of flow is reversed and the target

cells or other biological complexes are collected and subjected to molecular analysis preferably without further purification steps.

In molecular analytical techniques, such as immunoassays and nucleic acid assays, pre-analytical processing of samples is of utmost importance. To analyse e.g. the protein and/or nucleic acid content of a sample, it is often necessary to purify and to concentrate the sample, otherwise it is impossible to determine the amount or mere presence of the specific analyte of interest in the sample. This is typically due to either presence of assay inhibitors in the sample or low concentration of analyte or both. Most sample preparation methods, reviewed e.g. by Rådström et al. (2003), are limited by the fact that they are time-consuming and labour intensive and require specialized equipment, operator skills and harsh chemicals.

The present invention provides a simple method for sample purification and enrichment that is amenable to automated or manual use. The general principle of the method is depicted in figures 1 and 2. As can be seen from these figures, the technique is based on separation of biological particles 4, e.g. cells, containing the molecules of interest from the sample matrix using a filter 6. Optionally, the sample 2 can be pre-filtered before application to the main filter 6 in order to remove larger particles 10 (figure 2) that might interfere with the analysis of the analyte or analytes. As the biological particles 4 of interest are trapped on and/or in the filter 6, any interfering substances, such as compounds that could inhibit the subsequent analytical steps, pass through. After the entire volume of sample 2 has been forced through the filter 6, the biological particles 4 of interest can be optionally washed by e.g. applying a suitable volume of water or other liquid through the filter 6 (figure 2). After this first step, the direction of flow 8 is reversed so that the trapped particles 4 are detached from the filter 6. This second flush volume can be adjusted so that the particles 4, now purified from inhibitors, are flushed in a volume that is smaller than the initial sample volume, therefore resulting in effective enrichment or concentration of the analyte. The force and

volume of the reverse flush flow 8 can be adjusted so that all or nearly all trapped analyte containing biological particles 4 are collected. This enables even quantitative analysis of the amount of particles 4 in the sample 2.

5 The flush flow 8 can be any flow, even that of the sample filtrate. Preferable it is, however, a liquid or gas flow other than the sample filtrate in order to avoid reintroducing components of the original sample that might interfere with the analysis of the analyte.

10 "Flush flow in a second opposite direction through the filter " as used herein means that the direction of flow in relation to the filter plane of the sample inlet side 16 of the filter 6 is changed so that the trapped particles are collected into the flush flow 8 filtrate after changing the direction of flow. As will be appreciated by those skilled in the art, this action can be accomplished in different ways. For example the position of the filter 6 can be changed so that the direction of flow in relation to the filter 6 changes; or the filter can remain stationary while direction of flow is  
15 changed; or the filter 6 and direction of flow can both be adjusted so that the same end result, collection of trapped biological particles 4, is achieved. The flush flow 8 can be directed toward the filter from any suitable direction, as long as it flows out from the filter on the sample inlet side 16 and the biological particles 4 contained in the sample 2 are first trapped in the filter 6 and then, after changing the flow  
20 direction, collected in the flush flow 8 filtrate.

In some applications, the sample 2 may contain interfering particles or inhibitor complexes 10 that are greater in size than the biological particles 4, e.g. cells, containing the molecular species of interest. In these cases, it is possible to perform a first filtration where the biological particles 4 of interest pass through the  
25 first filter 26 while the interfering greater particles 10 are trapped in the first filter 26. The filtrate of the first filter 26 containing e.g. the complexes of interest 4 is then forced through a second filter 6 that traps the e.g. complexes of interest while

any interfering substances, such as compounds that could inhibit the subsequent analytical steps, pass through. After this, the direction of flow through the second filter 6 is changed and the biological particles 4 of interest are collected and then subjected to analysis. Again, it is possible to adjust the volumes applied through the filters 26, 6 at the different steps to achieve optimal purity and concentration of the particles 4.

The method of the present invention can be performed manually using a manual filtration device and a manual device that allows application of material through the filter, suitably a syringe. Alternatively, the method of the present invention can be performed using an automated device that is designed to perform the physical actions necessary to force a sample through a filter; to reverse the direction of flow through the filter; and to collect the biological particles. Suitably, pressure or vacuum is used to force material through a filter.

The terms "biological particles" as used herein refer to prokaryotic or eukaryotic cells or spores or components thereof, viral particles or complexes containing protein and nucleic acid, or complexes containing protein or complexes containing nucleic acid as well as any combinations thereof. Biological particles can e.g. be bacteria or bacterial cells, plant pollen, mitochondria, chloroplasts, cell nuclei, viruses, phages, chromosomes or ribosomes.

Retention of the biological particles in the filter can be due to their size and/or due to their chemical properties. Typically retention is essentially due to either the size of the particles or the chemical properties of the particle.

Suitably, the biological particles purified and enriched according to the principle depicted in figures 1 and 2 can be analysed by a method that allows measurement of the presence or amount of a specific molecule in the particles. These methods include but are not limited to the following: the polymerase chain reaction (PCR),

reverse transcriptase polymerase chain reaction (RT-PCR), immunoassay, ligase chain reaction (LCR), oligonucleotide ligation assay (OLA), nucleic acid sequence based amplification (NASBA), strand displacement amplification (SDA), fluorescence *in situ* hybridization. A combination of methods can also be used.

- 5 Suitably, the biological particles are flushed with a liquid or a gas that is different from the liquid or gas originally present in the sample prior to forcing the sample through the filter. Alternatively, the biological particles are flushed with the same liquid or gas that was present in the sample prior to forcing the sample through the filter.
- 10 Suitably the method of the present invention can be used to detect a living and/or dead cell or virus; a peptide, a protein or complex thereof; a nucleic acid; or any combination thereof. Typically, the method of the present invention can be used to detect one or more of the following: a bacterium, a yeast, a mold, a eukaryotic cell or organism, a cancer cell, a virus (e.g. pathogenic), a nucleic acid, a ribonucleic acid (RNA), a deoxyribonucleic acid (DNA), a derivative of a nucleic acid, a peptide, a protein (e.g. hormone, growth factor, enzyme or part thereof) or a complex of protein and nucleic acid. The method can also be used to detect any combination thereof.
- 15

- Suitably, the method of the present invention is used for one or more of the following purposes: diagnostics, environmental monitoring, detection of biological warfare agents, forensics, detection of micro-organisms, monitoring of industrial processes, drug discovery, development of medicaments, development of nutraceuticals, product quality control.
- 20

- The invention also concerns a kit of parts, components and/or reagents for use in the method according to the invention. Such a kit comprises the arrangement according to the invention and additionally other parts, components and/or reagents for
- 25

performing the method. Additional other parts, components and/or reagents are typically tailored for a specific analysis or a group of specific analyses. The kit can comprise a set of essential parts, components and/or reagents, but need not comprise everything (but the sample) needed for the analysis or analyses. Preferably it  
5 comprises all the parts, components and/or reagents not otherwise available at the typical site of carrying out the specific analysis or analyses.

Figure 1 shows the basic principle of the invention. Analyte particles 4 are collected from a sample 2 by a filtration step. The flow through the filter 6 is then changed in such a way that pure analyte particles 4 are flushed by the flush flow 8 from the  
10 filter 6, ready for analysis.

Figures 2a and 2b show a schematic presentation of the principle of the invention used in a more complex way. Large sample contaminants 10 are removed from the sample 2 with optional pre-filtration using a pre-filter 26 after which the analyte particles 4 are collected from the sample 2 by filtration with a filter 6. Any small  
15 molecule contaminants from the sample that may have been retained on the filter 6 are removed by an optional washing step. The flow through the filter 6 is then reversed in such a way that pure analyte particles 4 are flushed from the filter by the flush flow 8 and the particles 4 are ready for analysis.

Figures 3a, 3b and 3c show the principle of a prototype automatic sample pre-treatment instrument utilizing the principles of the present invention. In figure 3a  
20 the sample 2 with its analyte containing biological particles 4 is first pumped along a flow channel 28 so that it passes through an optional pre-filter 26, which removes large sample contaminants. Next the sample 2 passes through a filter 6 from the sample inlet side 16 to the flush flow inlet side 18 in its housing 14 mounted on a  
25 filter holder rack 32 capable of rotation. Analyte particles 4 are thus bound on the filter 6. The filtrate of filter 6 is led to waste 38. In figure 3b the filter holder rack 32 is then optionally rotated in such a way that wash buffer 34 can be pumped through

a pipe 30 through the filter 6 from the sample inlet side 16 to the flush flow inlet side 18, removing small sample contaminants adhering to the filter 6. The filtrate of the wash buffer is led to waste 38. In figure 3b the filter holder rack 32 is finally rotated in such a way that buffer 36 for flushing can be pumped through the filter 6 in a reverse direction compared to the sample and wash buffer flow, i.e. from the flush flow inlet side 18 to the sample inlet side 16. Analyte particles 4 are thus flushed with the flush flow 8 and retrieved 24 pure and ready for analysis.

Figure 4 is a standard curve for the detection of *Listeria monocytogenes* from milk using the present invention for sample pre-treatment and real time PCR for analyte detection.

Figure 5 is a standard curve for the detection of *Listeria monocytogenes* from cheese using the present invention for sample pre-treatment and real time PCR for analyte detection.

Figure 6 is a standard curve for the detection of *Listeria monocytogenes* from salted salmon using the present invention for sample pre-treatment and real time PCR for analyte detection.

Figure 7 is a standard curve for the detection of *Bacillus subtilis* from Luria broth using the present invention for sample pre-treatment and real time PCR for analyte detection.

Figure 8 is a standard curve for the detection of *Bacillus subtilis* endospores from potato flour using the present invention for sample pre-treatment and real-time PCR for analyte detection.

Figure 9 is a picture of an agarose gel analysis of the PCR amplifications of an actin fragment from human blood leucocytes isolated with the method of the present invention. Lanes 1 and 8 are molecular weight standards (GeneRuler™ 100bp DNA Ladder, Fermentas Life Sciences, Lithuania) whereas lane 7 is a positive control and

lane 2 is a negative control. Lanes 3 to 6 are PCR reactions with 1, 1, 10 and 10  $\mu$ l of extracted leucocytes added, respectively. The results show that the 136 bp actin fragment gets amplified only in the presence of the extracted leucocytes.

## Methods

### 5 Bacterial strains

*Listeria monocytogenes* strain ATCC 7644 was used in examples 1–3. *Bacillus subtilis* strain 168 DE1 [Ebbola, D.J. and Zalkin, H. (1987) Cloning and Characterization of a 12-Gene Cluster from *Bacillus subtilis* Encoding Nine enzymes for de Novo Purine Nucleotide Synthesis. J. Biol. Chem. 262, 8274–8287]

10 was used in examples 4 and 5.

### Real-time PCR

The real-time PCR detection method used for the detection of analytes in the examples [Nurmi, J., Wikman, T., Karp, M. and Lövgren, T. (2002) High-Performance real-Time Quantitative RT-PCR Using Lanthanide Probes and a Dual-  
 15 Temperature Hybridisation Assay. Anal. Chem. 74, 3525–2532.] is based on environment sensitive terbium chelates that have greater fluorescence intensity when they are free in solution than when attached to single-stranded DNA. During the extension phase of PCR the 5'-3'-exonucleolytic DNA polymerase digests the lanthanide probe that is specifically hybridised to template DNA. This results in  
 20 fluorescence signal increase that is measured in a time-resolved manner with a Victor 1420 Multilabel counter (Perkin Elmer Life Sciences Wallac, USA). The small background fluorescence resulting from undigested lanthanide probes is further decreased with a QSY-7-labelled quencher probe that hybridises to the terbium probe in the measurement temperature. The thermal cycling was performed  
 25 with a Peltier Thermal Cycler (MJ Research, USA).



## Probe, quencher and primer sequences used in PCR reactions

Oligonucleotide	Sequence from 5' to 3' end	Label/position
<i>Listeria</i> probe	CGATTTTCATCCGCGTGTTTCTTTTCGTA	Tb / 5'
<i>Listeria</i> quencher	CGCGGATGAAATCG	QSY-7 / 3'
<i>Listeria</i> 5' primer	TGCAAGTCCTAAGACGCCA	None
<i>Listeria</i> 3' primer	CACTGCATCTCCGTGGTATACTAA	None
<i>Bacillus</i> probe	TTGATGTGATGGCTCCTGGCCA	Tb / 5'
<i>Bacillus</i> quencher	CCATCACATCAA	QSY-7 / 3'
<i>Bacillus</i> 5' primer	ATGGATGTTATCAACATGAG	None
<i>Bacillus</i> 3' primer	GAGTCGCCATGGACGTTT	None
Actine 5' primer	TGAAGTCTGACGTGGACATC	None
Actine 3' primer	CTTGATCTTCATTGTGCTGGG	None

Pre-culture of *Listeria monocytogenes*

Fresh *Listeria monocytogenes* cells were prepared as follows. An aliquot of 5 ml of brain heart infusion broth (Labema, Finland) was inoculated with *Listeria* cells and cultured overnight at 37 °C. Dilutions of these cultures were plated on nutrient agar plates (Labema) to determine the amount of *Listeria* cells in each batch.

## Examples

### Example 1

#### *Detection of *Listeria monocytogenes* from milk*

Ten fold dilutions of fresh overnight *Listeria monocytogenes* cultures were made to  
5 ½ Fraser broth (Labema). 20 µl of each dilution was mixed with 1 ml of milk (2 %  
fat content) and ½ Fraser to a total volume of 10 ml. The *Listeria* cells were then  
grown for 18 h at 30 °C. One ml samples of each of these cultures were filtered  
through a 5 µm pore-size pre-filter in order to remove large sample particles.  
*Listeria* cells were then collected on a 0.45 µm pore-size filter by passing the sample  
10 through it. The cells on filter were washed with 10 ml of 0.9 % NaCl, flow direction  
through the filter was reversed and the cells were flushed with 500 µl of sterile  
water. 5 µl of the eluate was used in PCR reactions as template. The PCR reactions  
had the following conditions: 1.25 U AmpliTaq Gold DNA Polymerase, 1xPCR  
buffer II and 5 mM MgCl<sub>2</sub> (Applied Biosystems, USA), 0.2 mM dNTPs  
15 (Amersham Biosciences, U.K.), 0.3 µM *Listeria* primers, 0.83 µM *Listeria* probe  
and 8.3 µM *Listeria* quencher in a total volume of 50 µl. The thermal cycling profile  
was 95 °C 10 min, 95 °C 15 s, 60 °C 1 min repeated for a total of 40 cycles. In the  
end of each of the last 20 cycles the temperature was briefly lowered to 35 °C for  
time-resolved fluorescence measuring. PCR results were plotted against plating  
20 results in order to obtain the standard curve presented in figure 4.

### Example 2

#### *Detection of *Listeria monocytogenes* from cheese*

The enrichment step was done like in example 1, except that instead of using milk,  
1 g of blue cheese (minced thoroughly with a blender) was mixed with the fresh  
25 *Listeria* cells and ½ Fraser broth. Two ml aliquots of each of the enriched samples

were filtered through a 5  $\mu\text{m}$  pore-size pre-filter in order to remove large sample particles. *Listeria* cells were then collected on a 0.45  $\mu\text{m}$  pore-size filter by passing the sample through it. The cells on filter were washed with 20 ml of 0.9 % NaCl, flow direction through the filter was reversed and the cells were flushed with 500  $\mu\text{l}$  of sterile 0.9 % NaCl. 5  $\mu\text{l}$  of the eluate was used in PCR reactions as template. The PCR analysis was done as in example 1. PCR results were plotted against plating results in order to obtain the standard curve presented in figure 5.

### Example 3

#### ***Detection of *Listeria monocytogenes* from fish***

10 The enrichment step was done like in example 1, except that instead of using milk, 1 g of salted salmon (minced thoroughly with a blender) was mixed with the fresh *Listeria* cells and  $\frac{1}{2}$  Fraser broth. Two ml samples of each of these cultures were filtered through a 5  $\mu\text{m}$  pore-size pre-filter in order to remove large sample particles. *Listeria* cells were then collected on a 0.45  $\mu\text{m}$  pore-size filter by passing the sample  
15 through it. The cells on filter were washed with 10 ml of 0.9 % NaCl, flow direction through the filter was reversed and the cells were flushed with 500  $\mu\text{l}$  of sterile water. 5  $\mu\text{l}$  of the eluate was used in PCR reactions as template. The PCR analysis was done as in example 1. PCR results were plotted against plating results in order to obtain the standard curve presented in figure 6.

### 20 Example 4

#### ***Detection of *Bacillus subtilis* from LB growth medium***

*Bacillus subtilis* cells grown overnight in 2.5 ml of LB- medium (10 g tryptone, 5 g yeast extract and 10 g NaCl per liter, pH 7.0) were serially diluted to LB-medium. One ml of each dilution was filtered through a 0.22  $\mu\text{m}$  pore size filter. The cells on  
25 filter were washed with 1 ml of sterile water, the flow direction through the filter

was reversed and the cells were flushed with 0.5 ml of sterile water. 5 µl of the eluate was used as template in PCR reactions that had the following conditions: 1.5 U AmpliTaq Gold DNA Polymerase, 1xPCR buffer II and 6.5 mM MgCl<sub>2</sub> (Applied Biosystems, US), 0.8 mM dNTPs (Amersham Biosciences), 0.5 µM *Bacillus* primers, 1.7 µM *Bacillus* probe and 41.5 µM *Bacillus* quencher in a total volume of 50 µl. The thermal cycling profile was 95 °C 10 min, 95 °C 15 s, 53 °C 30 s and 61°C 30 s repeated for a total of 40 cycles. In the end of each of the last 20 cycles the temperature was briefly lowered to 35 °C for time-resolved fluorescence measuring. The amount of *Bacillus* cells in each of the serial dilutions was determined with platings. PCR results were plotted against plating results in order to obtain the standard curve presented in figure 7.

#### Example 5

##### ***Detection of Bacillus subtilis endospores from potato flour***

Dilutions of *Bacillus subtilis* spores were made to Ringer solution (8.6 g NaCl, 0.3 g KCl, 0.48 g CaCl<sub>2</sub> per liter) containing 10 % potato flour suspension. The dilutions were first prefiltered through 5 µm pore size filters and then the cells were collected by passing the samples through 0.45 µm pore size filters. The spores on filter were washed with 1 ml of sterile water, the flow direction through the filter was reversed and the spores were flushed with 1 ml of sterile water. 5 µl of the eluate was added to PCR reactions as template. The PCR analysis was done as in example 4. The amount of *Bacillus* spores in each of the samples was determined with platings. PCR results were plotted against plating results in order to obtain the standard curve presented in figure 8.

Example 6*Extraction of leucocytes from whole blood*

An aliquot of 300  $\mu$ l of whole EDTA blood was mixed with 900  $\mu$ l of 20 mM Tris-HCl, pH 7.5 in order to lyse the red blood cells. Leucocytes were then collected by  
5 filtration through a 5  $\mu$ m pore size filter. The leucocytes on the filter were washed with 3 ml of the above buffer, the flow direction through the filter was reversed and the cells flushed from the filter with 1 ml of sterile water. Aliquots from 1 to 10  $\mu$ l were used as templates in 50  $\mu$ l PCR reactions that contained 2.0 U AmpliTaq Gold DNA Polymerase, 1xPCR buffer II, 3.5 mM  $MgCl_2$ , 0.2 mM dNTPs and 0.5  $\mu$ M  
10 Actine primers. The thermal cycling profile was 95  $^{\circ}C$  10 min, 95  $^{\circ}C$  30 s, 60  $^{\circ}C$  30 s and 72  $^{\circ}C$  30 s repeated for a total of 40 cycles. The PCR reactions were analyzed with agarose gel electrophoresis. The picture of the gel is shown in figure 9. The results show that the 136 bp actin fragment gets amplified only in the presence of the extracted leucocytes.

## CLAIMS

1. A method for preparing a biological sample (2) for quantitative and/or qualitative analysis of the presence of a specific analyte or specific analytes, which analytes, if present, are contained in biological particles (4) of the sample (2), in  
5 which method the sample (2) is forced in a first direction through a filter (6) that retains said biological particles (4) characterised in that said biological particles (4) retained in said filter (6) are flushed, by a flush flow (8), in a second opposite direction through said filter (6) out of said filter (6) and said flush flow (8) containing said biological particles (4) flushed out is analysed for the analyte or  
10 analytes.
2. The method of claim 1 characterised in that said method comprises an additional filtration prior to the filtration retaining the biological particles (4) containing the analyte or analytes, which additional filtration does not retain the biological particles (4) containing the analyte or analytes but retains particles (10)  
15 that might interfere with the analysis of the analyte or analytes.
3. The method of claim 1 or 2 characterised in that the flow containing the biological particles (4) containing the analyte or analytes flushed out is analysed for the analyte or analytes without any further purification.
4. The method of claim 1, 2 or 3 characterised in that retention of the  
20 biological particles (4) containing the analyte or analytes in the filter (6) is essentially size dependent.
5. The method of any of claims 1 to 4 characterised in that retention of the biological particles (4) containing the analyte or analytes in the filter (6) is essentially dependent on the chemical properties of the particle.

6. The method of any of claims 1 to 5 characterised in that the biological particles (4) containing the analyte or analytes are selected from the group consisting of prokaryotic or eukaryotic cells or spores or components thereof, viruses or viral particles, complexes comprising protein and/or nucleic acid, and any combination thereof.
7. The method of claim 6 characterised in that the biological particles (4) containing the analyte or analytes are selected from the group consisting of bacteria, bacterial cell, plant pollen, mitochondria, chloroplast, cell nuclei, virus, phage, chromosome and ribosome.
8. The method of any of claims 1 to 7 characterised in that the means of analysing the analyte or analytes is selected from the group consisting of immunoassay, polymerase chain reaction (PCR), reverse transcriptase polymerase chain reaction (RT-PCR), ligase chain reaction (LCR), oligonucleotide ligation assay (OLA), nucleic acid sequence based amplification (NASBA), strand displacement amplification (SDA), fluorescence *in situ* hybridisation, and any combination thereof.
9. The method of any of claims 1 to 8 characterised in that the biological particles (4) containing the analyte or analytes are flushed with a liquid or a gas preferably not contained in the original sample 2.
10. The method of any of claims 1 to 9 characterised in that the analyte or analytes are selected from the group consisting of a living and/or dead cell or virus; a peptide, a protein or complex thereof; a nucleic acid; and any combination thereof.

11. The method of claim 10 characterised in that the analyte or analytes comprises living and/or dead cells and/or viruses selected from the group consisting of a mold, a yeast, a eukaryotic cell or organism, a pathogenic virus and a cancer cell.
- 5 12. The method of claim 10 characterised in that the analyte or analytes comprises nucleic acids selected from the group consisting of DNA, RNA and any derivative thereof.
13. The method of claim 10 characterised in that the analyte or analytes comprises peptides and/or proteins or complexes thereof selected from the group  
10 consisting of a hormone, a growth factor, an enzyme or parts thereof and/or complexes thereof; and any combination thereof.
14. An arrangement (12) for preparing a biological sample (2) for quantitative and/or qualitative analysis of the presence of a specific analyte or specific analytes, which analytes, if present, are contained in biological particles (4) of the sample (2),  
15 characterised in that the arrangement (12) comprises
- a) a housing (14) for a filter (6);
  - b) a filter (6) within said housing (14) for retaining the biological particles (4) containing the analyte or analytes, said filter (6) having two sides,
    - i) a sample inlet side (16) and  
20 ii) a flushing flow inlet side (18); and



c) means for

- i) leading (20) the sample (2) through the filter (6) from the sample inlet side (16) to the flushing flow inlet side (18),
- ii) leading (22) the flush flow (8) from its inlet side (18) to the sample inlet side (16), and
- iii) retrieving (24) for analysis biological particles (4) containing the analyte flushed from the filter (6).

15. The arrangement (12) according to claim 14 characterised in that the arrangement (12) further comprises

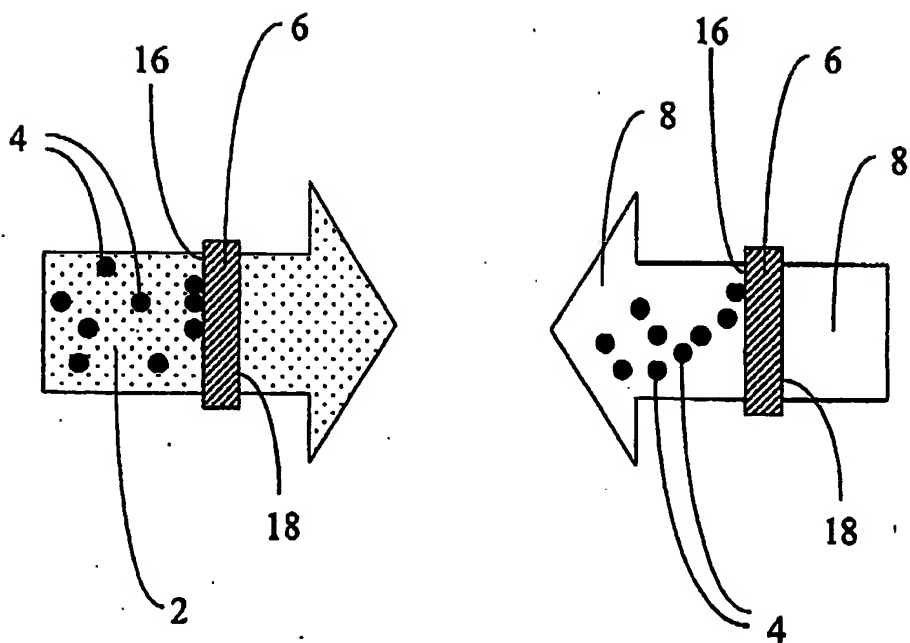
- a) an additional filter (26) that does not retain the biological particles (4) containing the analyte or analytes but retains particles (10) that might interfere with the analysis of the analyte or analytes, and
- b) means for leading (28) the sample (2) through said additional filter (26) prior to leading it through the filter (6) for retaining the biological particles (4) containing the analyte or analytes.

16. The arrangement (12) according to claim 14 or 15 characterised in that the arrangement (12) further comprises means for leading (30) a washing liquid or gas through the filter (6) from the sample inlet side (16) to the flushing flow inlet side (18) for washing the retained biological particles (4) containing the analyte or analytes prior to flushing them out of the filter (6).

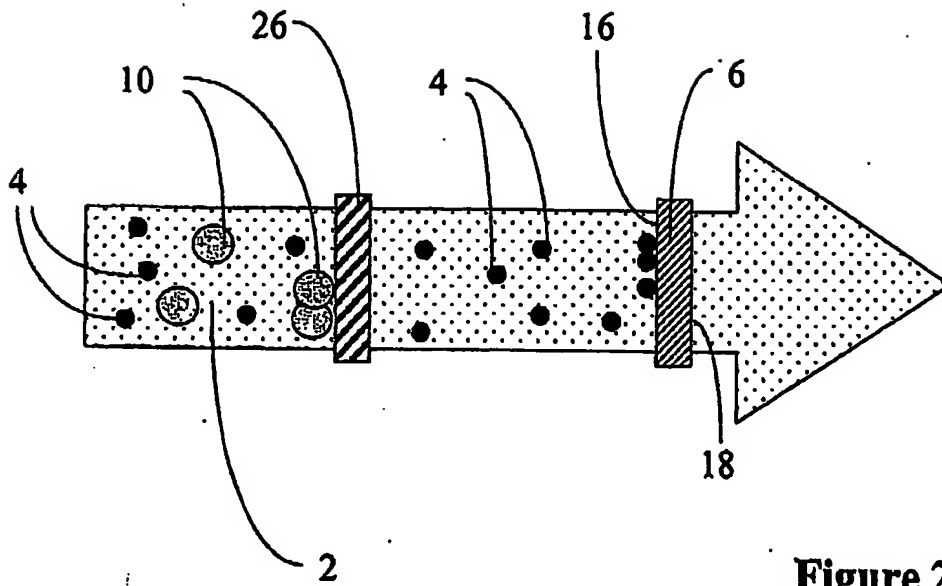
17. The arrangement (12) according to any of claims 14 to 16 characterised in that the arrangement (12) comprises a filter rack (32) that is a multi-way valve, with connections for sample inlet (20), sample retrieval (24), flush flow inlet (36) and waste disposal (38), and optionally for wash flow (34), and the filter rack (32) with the filter (6) can be turned in alternative positions so that flow is directed from
- a) the sample inlet (20) into the filter (6) from the sample inlet side (16) to the flush flow inlet side (18) and to waste (38) or optionally for use as flush flow,
  - b) the flush flow inlet (22) into the filter (6) from the flush flow inlet side (18) to the sample inlet side (16) and to sample retrieval (24), or optionally
  - 10 c) the flow inlet (30) into the filter (6) from the sample inlet side (16) to the flush flow inlet side (18) and to waste (38) or optionally for recycling.
18. A kit of parts, components and/or reagents for performing the method according to any of claims 1 to 13 characterised in that it comprises the arrangement (12) according to any of claims 15 to 17.

**ABSTRACT**

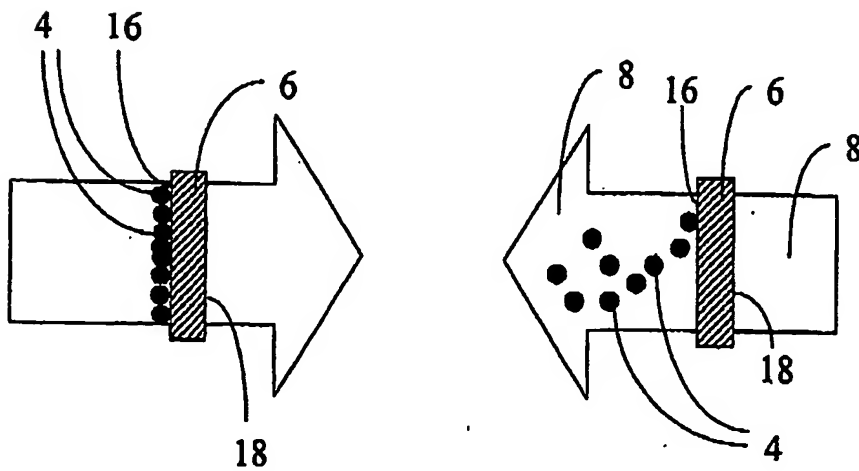
The present invention relates to a method for preparing a biological sample (2) for quantitative and/or qualitative analysis of the presence of a specific analyte or specific analytes, which analytes, if present, are contained in particles (4) of the sample (2), in which method the sample is forced in a first direction through a filter (6) that retains said particles (4). Characteristic for the method is that the particles (4) retained in the filter (6) are flushed, by a flow (8), in a second opposite direction through the filter (6) out of the filter (6) and the flow (8) containing said particles (4) flushed out is analysed for the analyte or analytes. The invention further relates to an arrangement (12) for preparing the sample (2) according to the method of the invention and to a kit of parts for analysing the analyte or analytes, which kit comprises the arrangement (12).



**Figure 1**



**Figure 2a**



**Figure 2b**

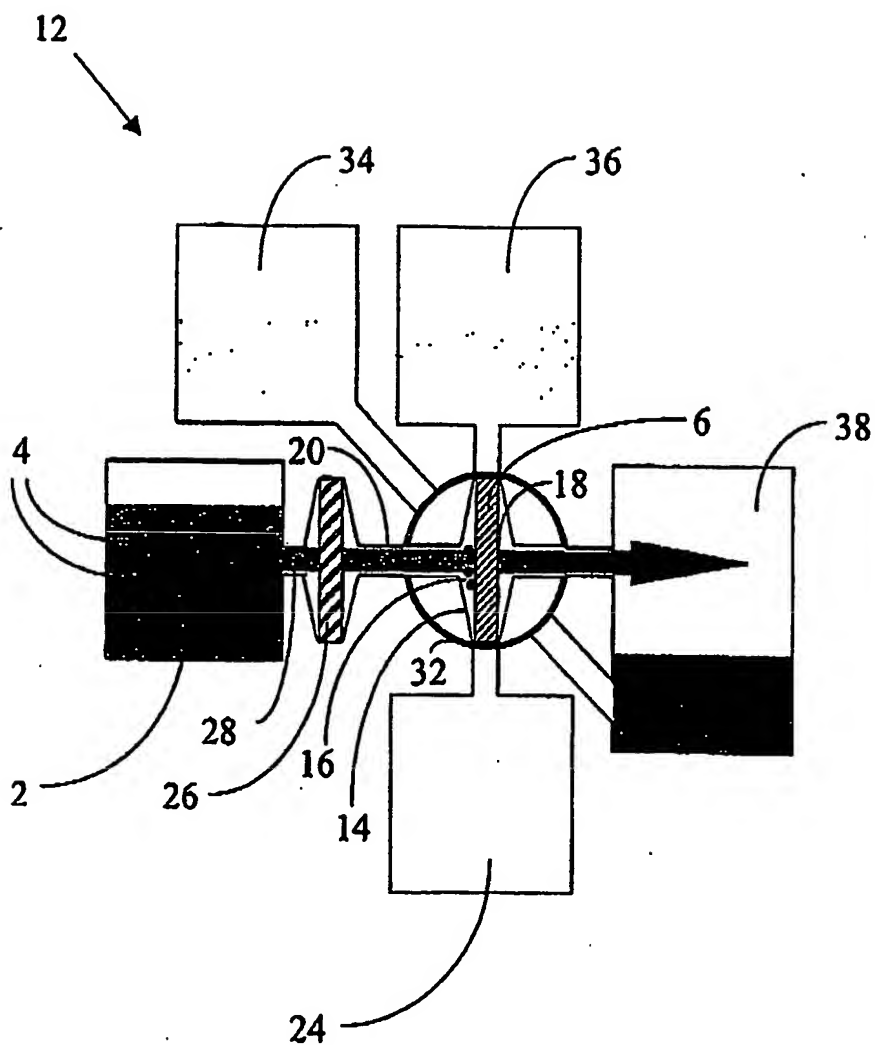

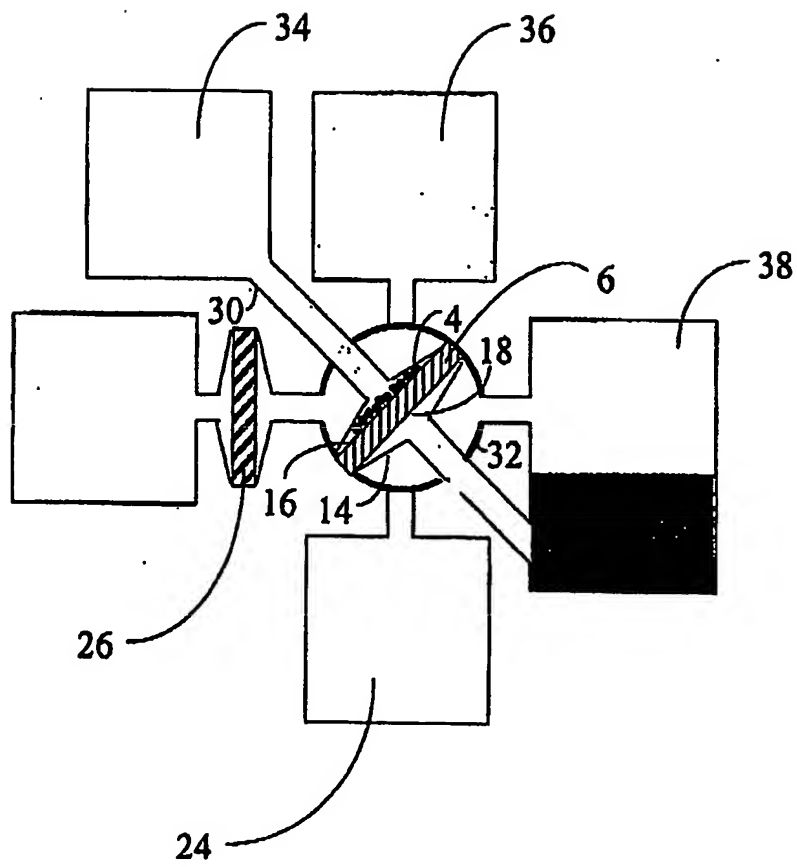
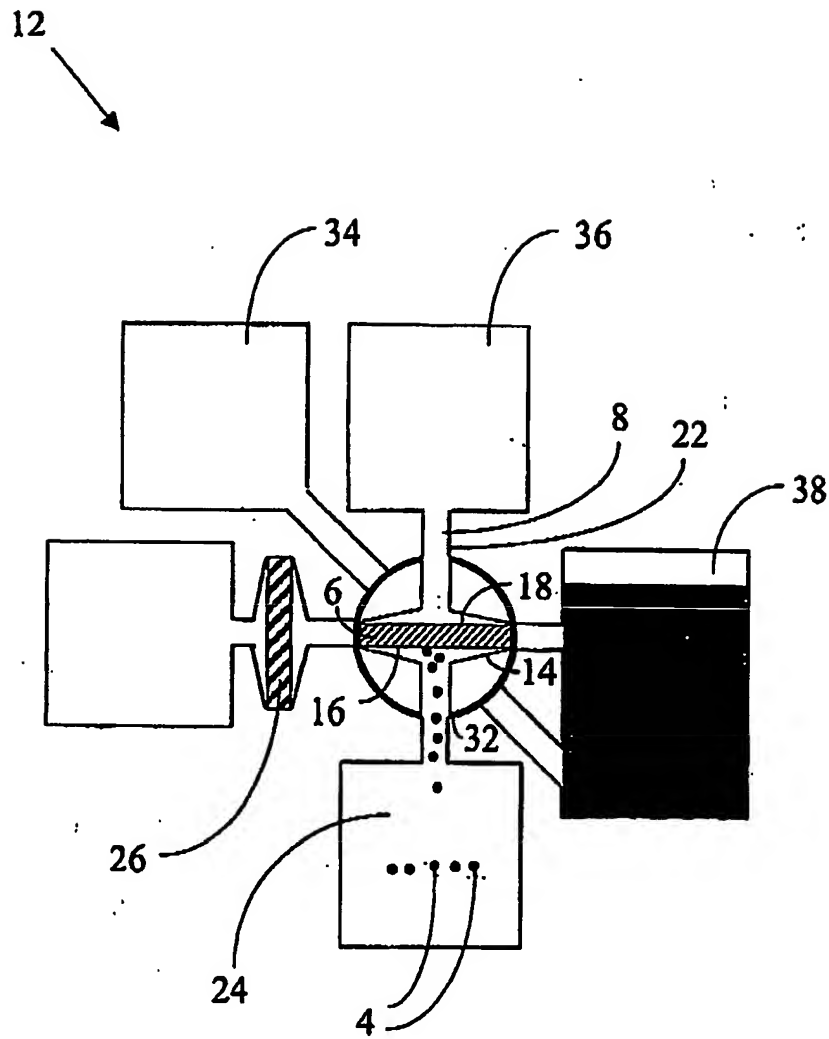


Figure 3a

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**Figure 3b**



**Figure 3c**



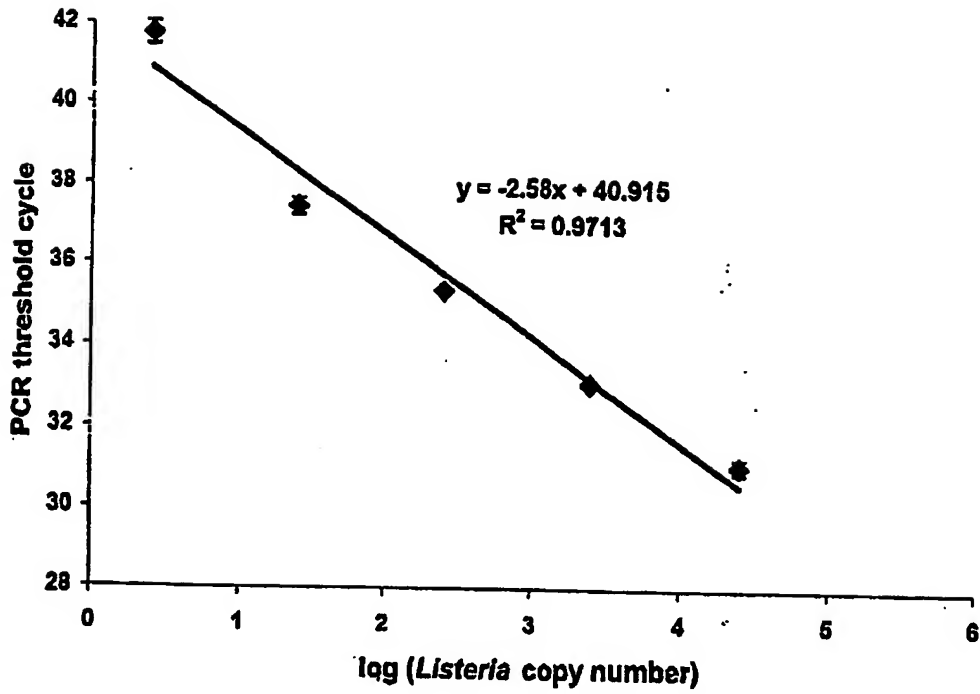


Figure 4

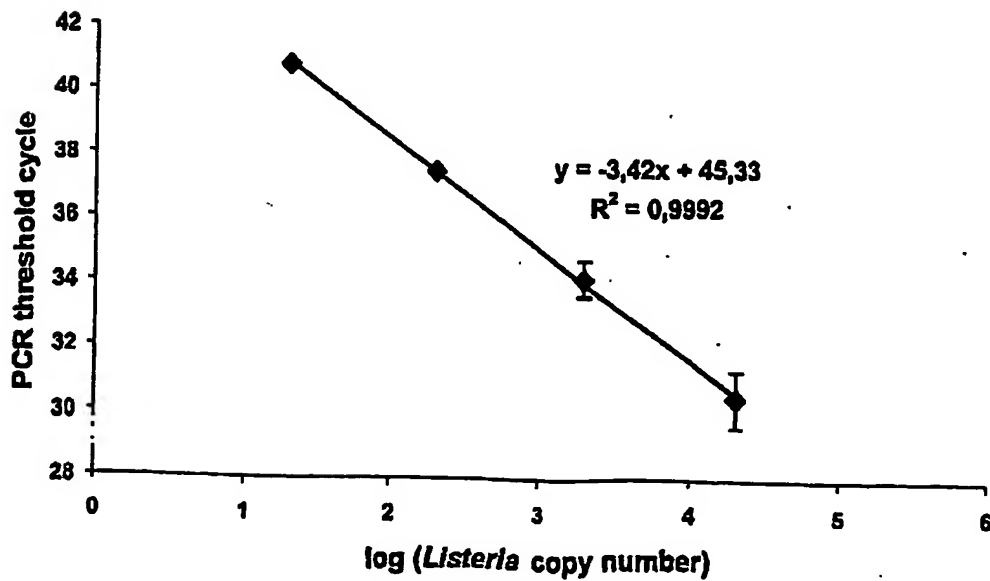


Figure 5

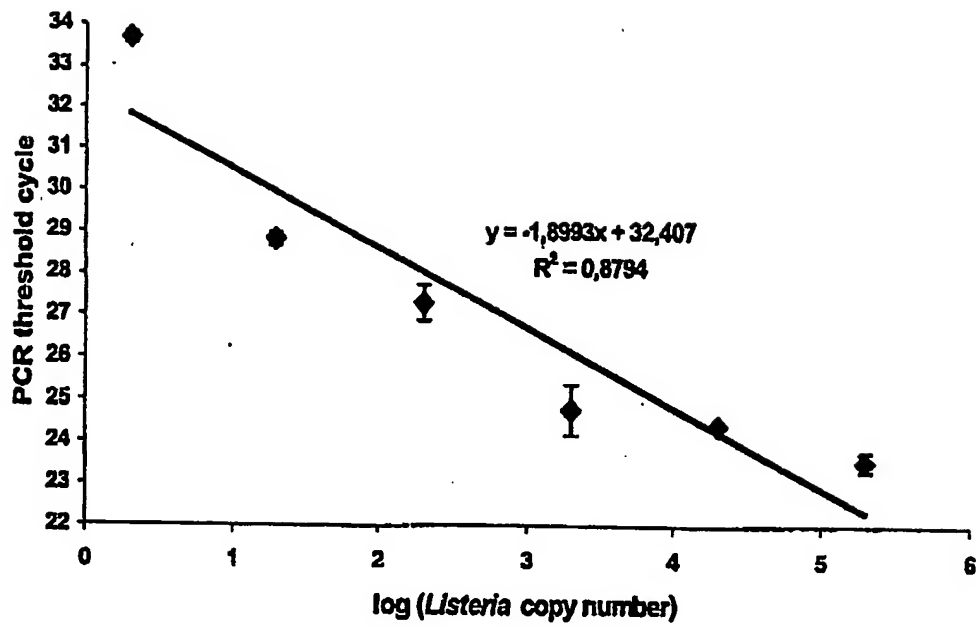


Figure 6

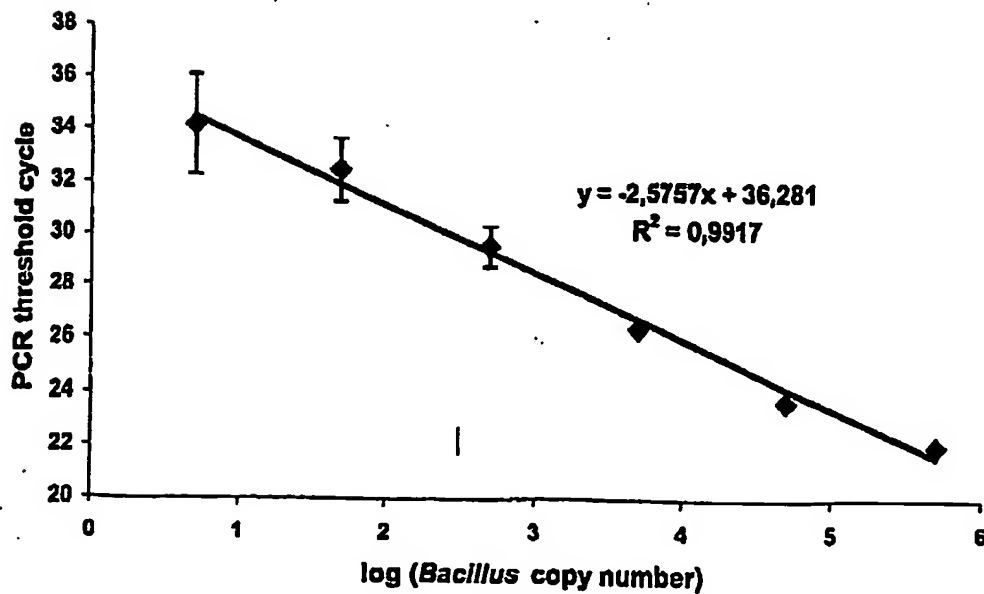


Figure 7

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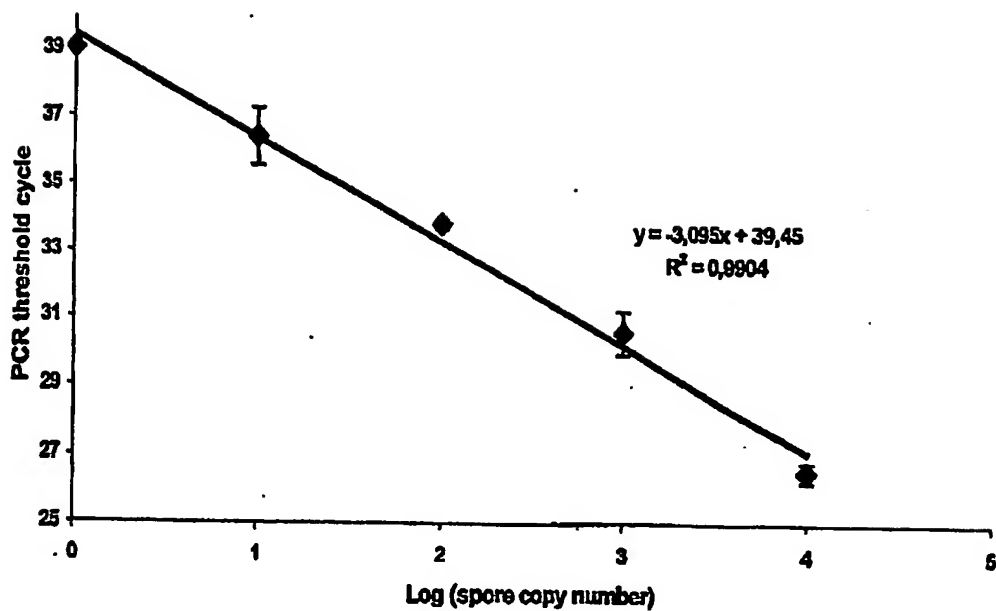


Figure 8

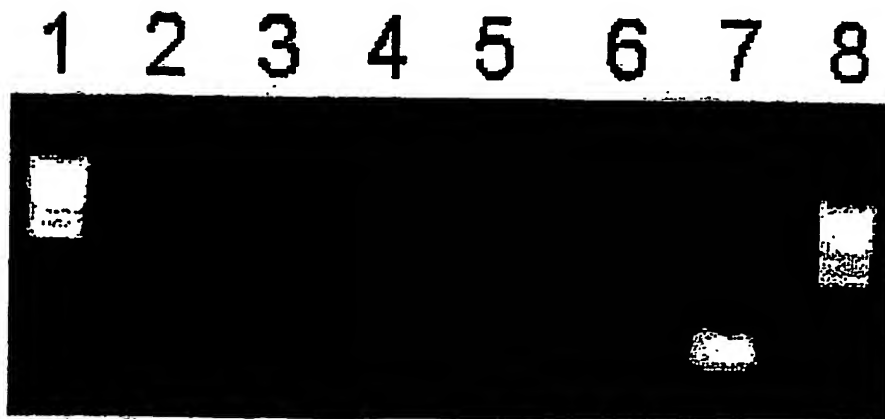


Figure 9

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